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TECH CENTER 1600/2000

ENTERED #27

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/08/765,588A

DATE: 02/01/2001
 TIME: 12:12:02

Input Set : A:\sequence.asc
 Output Set: N:\CRF3\02012001\H765588A.raw

4 <110> APPLICANT: Hayward, Nicholas K.
 5 Weber, Gunther
 6 Grimmond, Sean
 7 Nordenskjold, Magnus
 8 Larsson, Catharina
 10 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
 11 SAME
 13 <130> FILE REFERENCE: DAVIES
 15 <140> CURRENT APPLICATION NUMBER: 08/765,588A
 C--> 16 <141> CURRENT FILING DATE: 1997-04-27
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 649
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Nucleotide Sequence of VEGF165
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (17)..(589)
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 35 1 5 10
 37 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
 39 Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 40 15 20 25
 42 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
 44 Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 45 30 35 40
 47 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
 49 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 50 45 50 55 60
 52 atc ttc cag gag tac ctc gat gag atc gag tac atc ttc aag cca tcc 244
 54 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
 55 65 70 75
 57 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
 59 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 60 80 85 90
 62 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
 64 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 65 95 100 105
 67 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cay 388
 69 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 70 110 115 120
 72 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
 74 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 75 125 130 135 140

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77 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat tlg ttt gta caa 484
 79 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 80 145 150 155
 82 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
 84 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 85 160 165 170
 87 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
 89 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
 90 175 180 185
 92 ccg agg cgg tgagccgggc aggaggaagg aycctccctc agcgttcgg 629
 94 Pro Arg Arg
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 97 gaaccagatc tctcaccagg 649
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 103 <212> TYPE: PRT
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 110 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 111 20 25 30
 113 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 114 35 40 45
 116 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 117 50 55 60
 119 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 120 65 70 75 80
 122 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 123 85 90 95
 125 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 126 100 105 110
 128 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 129 115 120 125
 131 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 132 130 135 140
 134 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 135 145 150 155 160
 137 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 138 165 170 175
 140 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 141 180 185 190
 145 <210> SEQ ID NO: 3
 146 <211> LENGTH: 1094
 147 <212> TYPE: DNA
 148 <213> ORGANISM: Nucleotide Sequence of SOM175
 150 <220> FEATURE:
 151 <221> NAME/KEY: CDS
 152 <222> LOCATION: (3)..(623)

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 158 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 159 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 160 20 25 30
 161 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 162 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 163 35 40 45
 164 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 165 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 166 50 55 60
 167 gtg gcc aaa cug ctg gtg ccc aqc tgc gtg act gtg cag cgc tgt ggt 239
 168 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 169 65 70 75
 170 ggc tgc tgc cct gac gat ggc ctg gag tgt gtc ccc act ggg cag cac 287
 171 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 172 80 85 90 95
 173 caa gtc cgg atg cag atc ctc atq atc cgg tac ccc agc aqt cag ctg 335
 174 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 175 100 105 110
 176 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 177 Gly Glu Met Ser Leu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 178 115 120 125
 179 aaa aag gac aqt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
 180 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
 181 130 135 140
 182 cgt ccc cag ccc cgt tct gtt ccc ggc tgg gac tct gcc ccc gga gca 479
 183 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
 184 145 150 155
 185 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
 186 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
 187 160 165 170 175
 188 gcc cac gct gca ccc agc acc acc agc ggc ctg acc ccc gga cct gcc 575
 189 Ala His Ala Ala Pro Ser Thr Ser Ala Leu Thr Pro Gly Pro Ala
 190 180 185 190
 191 gct gcc gct gcc gac gca gct tcc tcc gtt gcc aag ggc ggg gct 623
 192 Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 193 195 200 205
 194 tagagctaa cccagacacc tgcagggtgcc gggagctgct aqgggtgacac atggcttttc 683
 195 agactcagca ggggtgacttg cctcagaggc tataatcccg tggggggaca aagggggagcc 743
 196 tggtaaaaaa cagccaaagcc cccaaagacct cagccccaggc agaaqctgct ctggacactg 803
 197 ggcctctcag agggctcttc tgcctatccct tgcctccctg agggccatcat caaacaggac 863
 198 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct cagggggaaa 923
 199 tggatgtactg ttcctatccctt taaccactct gtgcagttaa gcatcttaca actggctt 983
 200 ctcctccctca ctaagaagac ccaaaacctct gctataatggg atttgggtt tggataaga 1043
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RAW SEQUENCE LISTING
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Input Set : A:\sequence.asc
 Output Set: N:\CRF3\02012001\H765588A.raw

246 <211> LENGTH: 207
 247 <212> TYPE: PRT
 248 <213> ORGANISM: Nucleotide Sequence of SOM175
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 254 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 255 20 25 30
 257 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 258 35 40 45
 260 Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 261 50 55 60
 263 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 264 65 70 75 80
 266 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 267 85 90 95
 269 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 270 100 105 110
 272 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 273 115 120 125
 275 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 276 130 135 140
 278 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 279 145 150 155 160
 281 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 282 165 170 175
 284 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 285 180 185 190
 287 Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 288 195 200 205
 292 <210> SEQ ID NO: 5
 293 <211> LENGTH: 993
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
 297 <220> FEATURE:
 298 <221> NAME/KEY: CDS
 299 <222> LOCATION: (3)..(566)
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 305 1 5 10 15
 307 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 309 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 310 20 25 30
 312 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 314 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 315 35 40 45
 317 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 319 Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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324	Val	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
325	65					70				75							
327	ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	287
329	Gly	Cys	Cys	Pro	Asp	Asp	Cys	Cys	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His
330	80				85				90				95				
332	caa	gtc	cgg	atg	cag	atc	ctc	atg	atc	egg	tac	ccg	agc	agt	cag	ctg	335
334	Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
335	100				105				105				110				
337	ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	383
339	Gly	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
340	115				120				120				125				
342	aaa	aag	gac	agt	gtg	aag	cca	gat	agc	ccc	agg	ccc	ctc	tgc	cca	431	
344	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	
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347	cgc	tgc	acc	cag	cac	cac	cag	cgc	cct	gac	ccc	cgg	acc	tgc	cgc	tgc	479
349	Arg	Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	
350	145				150				150				155				
352	cgc	tgc	cga	cgc	cgc	agc	ttc	ctc	cgt	tgc	caa	ggg	cgg	ggc	tta	gag	527
354	Arg	Cys	Arg	Arg	Arg	Ser	Phe	Ieu	Arg	Cys	Gln	Gly	Arg	Gly	Ieu	Glu	
355	160				165				170				175				
357	ctc	aac	cca	gac	acc	tgc	agg	tgc	cgg	aag	ctg	cga	agg	tgacacatgg		576	
359	Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg				
360	180				185				185								
362	cttttcagac	tcagcagggt	gacttgctc	agaggctata	tccca	gtgggg	ggaa	acaa	agg								636
365	ggagcctgg	aaaaaacgc	caaggccccca	agac	ctc	agc	ccagg	cgaa	gtgt	ctcg							696
368	gac	ctgg	ggcc	tctc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc		756
371	caggac	acag	ttggaa	aggagg	agact	gggg	gca	caag	agag	gggt	tcacata	ccag	tcagg				816
374	ggagaatgg	gtactgt	tgc	atgtt	ctaa	cact	tcgt	gc	aact	taag	cat	ttt	acaact	g			876
377	gtcttc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc		936
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396	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln	
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399	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val	
400							50		55			60					
402	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	
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405	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	
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VERIFICATION SUMMARY
PATENT APPLICATION: US/08/765,588A

DATE: 02/01/2001
TIME: 12:12:03

Input Set : A:\sequence.asc
Output Set: N:\CRF3\02012001\H765588A.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date